```
OM protein - nucleic search, using frame_plus_p2n model

Run on:          January 16, 2003, 16:51:22 ; Search time 81.8571 Seconds
                                              (without alignments)
                                              137.557 Million cell updates/sec

Title:           US-09-856-070-25
Perfect score:   23
Sequence:        1 MLRLQ 5

Scoring table:   BLOSUM62
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                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:       4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing  Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09856070/runat_14012003_155833_1611/app_query.fasta_1.1592
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856070_@CGN_1_1_448_@runat_14012003_155833_1611 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_101002.*
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23	100.0	27	19	AAV59481	Bacillus sp. pecti
	2	23	100.0	36	19	AAV21259	Tissue plasminogen
	3	23	100.0	51	22	AAS60687	Human cancer agent
	4	23	100.0	51	22	AAI77674	Human silent SNP c
	5	23	100.0	60	24	ABN34918	Human spliced tran
	6	23	100.0	60	24	ABN43764	Human spliced tran
c	7	23	100.0	73	16	AAT25114	Human gene signatu
	8	23	100.0	91	22	AAS04515	Gene expression pr
c	9	23	100.0	91	22	AAS04706	Gene expression pr
c	10	23	100.0	103	21	AAC14334	Human secreted pro
c	11	23	100.0	112	21	AAC17085	Human secreted pro
c	12	23	100.0	112	21	AAA45803	Human secreted exp
	13	23	100.0	129	24	ABK76832	Bacillus lichenifo
c	14	23	100.0	134	22	AAH37077	Human colon cancer
	15	23	100.0	139	22	ABA35126	Probe #13592 for g
	16	23	100.0	152	24	ABL77241	Human ovarian canc
	17	23	100.0	173	22	AAS04691	Gene expression pr
	18	23	100.0	182	21	AAA87256	Rat hepatocyte car
c	19	23	100.0	191	21	AAA41472	Human secreted exp
	20	23	100.0	210	22	AAS35154	Human cardiovascul
	21	23	100.0	210	22	AAK59784	Human immune/haema
c	22	23	100.0	211	21	AAC29479	Human secreted pro
	23	23	100.0	218	22	AAK65547	Human immune/haema
c	24	23	100.0	219	22	ABA72579	Human foetal liver
c	25	23	100.0	219	22	AAK21096	Human brain expres
c	26	23	100.0	219	22	AAK47158	Human bone marrow
c	27	23	100.0	219	22	AAI52994	Probe #21680 used
c	28	23	100.0	239	21	AAC06295	Human secreted pro
c	29	23	100.0	249	21	AAA41526	Human secreted exp
c	30	23	100.0	249	22	AAS35687	Human cardiovascul
c	31	23	100.0	255	22	AAH82158	Rat differential t
	32	23	100.0	256	19	AAV55848	Nucleotide sequenc
	33	23	100.0	256	21	AAA30937	Human Expressed se
	34	23	100.0	259	24	ABL38206	Human colon tumour
c	35	23	100.0	259	24	ABL36700	Human colon tumour
c	36	23	100.0	265	16	AAT21149	Human gene signatu
	37	23	100.0	267	24	ABK77674	Bacillus clausii g
c	38	23	100.0	273	22	AAK64746	Human immune/haema
c	39	23	100.0	273	22	AAK64748	Human immune/haema
c	40	23	100.0	273	22	AAK64752	Human immune/haema
c	41	23	100.0	274	22	AAS39574	cDNA encoding nove
c	42	23	100.0	274	22	AAK88913	Human digestive sy
	43	23	100.0	274	24	ABN22970	Human CREX polynuc
	44	23	100.0	279	22	AAK68146	Human immune/haema
	45	23	100.0	279	22	AAK68147	Human immune/haema

ALIGNMENTS

```
RESULT 1
AAV59481
ID   AAV59481 standard; DNA; 27 BP.
XX
AC   AAV59481;
XX
DT   07-JAN-1999  (first entry)
XX
DE   Bacillus sp. pectic acid lyase mutagenic PCR primer Cys71Ala.
XX
KW   Bacillus sp. KSM P15; pectic acid lyase; pectinic acid lyase; pectin;
KW   detergent; food-processing; fibre processing agent; cell wall;
KW   PCR primer; mutagenic; ss.
XX
OS   Synthetic.
OS   Bacillus sp.
XX
PN   EP870834-A1.
```

XX
PD 14-OCT-1998.
XX
PF 09-APR-1998; 98EP-0106586.
XX
PR 08-SEP-1997; 97JP-0242735.
PR 09-APR-1997; 97JP-0091142.
XX
PA (KAOS) KAO CORP.
XX
PI Hatada Y, Ito S, Kobayashi T, Koike K, Suzumatsu A;
PI Yoshimatsu T;
XX
DR WPI; 1998-523159/45.
XX
PT New Bacillus pectic acid lyase useful as a detergent component, a
PT food-processing agent and a fibre-processing agent
XX
PS Example 14; Page 11; 29pp; English.
XX
CC The present sequence represents a mutagenic PCR primer used for
CC introducing mutations into the pectic acid lyase isolated from
CC microorganism Bacillus sp. KSM-P15, of the present invention. The pectic
CC acid lyase has high pectic acid lyase activity which degrades pectin in
CC plant cell walls and fibre in vegetables, and so is useful as a
CC component of detergents, a food-processing agent, or a fibre-processing
CC agent. The pectic acid lyase has a higher optimum reaction pH (10.3-10.7)
CC than known Bacillus pectic acid lyases (pH 8-9.5) and so has wider
CC industrial applications. Unlike present pectic acid lyases, the new
CC enzyme has a high enzyme activity, and can be produced on a mass scale.
XX
SQ Sequence 27 BP; 8 A; 5 C; 7 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	115	Length:	27
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-856-070-25 (1-5) x AAV59481 (1-27)

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Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db       8 ATGCTACGATTACAA 22
```

RESULT 2
AAV21259
ID AAV21259 standard; DNA; 36 BP.
XX
AC AAV21259;
XX
DT 07-JUL-1998 (first entry)
XX
DE Tissue plasminogen activator mutation primer 10.
XX
KW tPA; fibrin-stimulated, clot, treatment, vascular disease; ss;
KW fibrin deposition; adhesion formation; primer.
XX
OS Synthetic.
XX
PN US5714145-A.
XX
PD 03-FEB-1998.
XX
PF 02-SEP-1988; 88US-0240856.
XX
PR 24-JUL-1989; 89US-0383608.
PR 02-SEP-1988; 88US-0240856.
PR 03-OCT-1991; 91US-0770510.
PR 06-JUL-1993; 93US-0088451.
PR 07-JAN-1994; 94US-0179059.
PR 14-APR-1995; 95US-0422736.
PR 29-MAR-1996; 96US-0622891.
PR 17-OCT-1996; 96US-0733353.
XX
PA (GEIH) GENENTECH INC.
XX
PI Anderson S, Bennett WF, Botstein D, Higgins DL;
PI Paoni NF, Zoller MJ;
XX
DR WPI; 1998-129803/12.
XX
PT Treatment of vascular conditions or disease - using tissue
PT plasminogen activator variant having amino acid substitutions in
PT protease domain to increase fibrin specificity
XX
PS Example 2; Column 27-28; 31pp; English.
XX
CC Primers AAV21250-V21281 were used to create mutant t-PA constructs, such
CC as variant AAW52817, where amino acids were substituted with alanine.
CC The t-PA variants (AAW52814-W52817) created by this method and deletion
CC mutations have a higher fibrin-stimulated activity than
CC fibrinogen-stimulated activity so they will act preferentially at the
CC site of a clot and not systemically. They can be used for treating
CC vascular diseases and conditions or to prevent fibrin deposition or
CC adhesion formation or reformation.
XX
SQ Sequence 36 BP; 9 A; 7 C; 8 G; 12 T; 0 other;

Alignment Scores:

Pred. No.:	157	Length:	36
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-856-070-25 (1-5) x AAV21259 (1-36)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db      15 ATGCTGCGACTGCAA 29
```

RESULT 3
AAS60687
ID AAS60687 standard; cDNA; 51 BP.
XX
AC AAS60687;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human cancer agent resistance marker #442.
XX
KW Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
KW squamous cell carcinoma, sarcoma, fibrosarcoma; leukaemia;
KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
KW Hodgkin's disease; glioma; ss.
XX
OS Homo sapiens.
XX
PN WO200179556-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US12132.
XX
PR 14-APR-2000; 2000US-197538P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Brown JL, Bolt A, Van Huffel C;
XX
DR WPI; 2001-602933/68.
XX

```
PT   Novel nucleic acid, used as a marker to determine the effectiveness of
PT   using TAXOL to treat cancer cell growth in individuals -
XX
PS   Claim 1, Page 276, 527pp, English.
XX
CC   The invention relates to 1046 novel nucleic acids which are used as
CC   markers for determining the sensitivity of a cancer cell to the
CC   anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC   they are shown to express one of the 242 sensitivity markers or the
CC   cells are shown not to express one of the 804 resistance markers.
CC   The methods can be used to determine the effectiveness of TAXOL
CC   in the treatment of cancer cell growth in an individual. The markers
CC   can be used as targets in developing anti-cancer agents such as
CC   chemotherapeutic compounds. The markers can also be used as targets in
CC   developing treatments for cancer, particularly those cancers which
CC   display resistance to agents and exhibit expression of the markers. The
CC   anticancer agents developed by the novel method can be used to treat
CC   cancer. Probes based on the markers can be used to detect transcripts or
CC   genomic sequences corresponding to the markers, in the identification of
CC   cells or tissues which mis-express the protein. Cancers which may
CC   be targeted include carcinoma (e.g. squamous cell carcinoma),
CC   sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
CC   lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and
CC   tumours (e.g. glioma). The present sequence is one of the 1046
CC   novel cancer cell markers.
XX
SQ   Sequence 51 BP, 10 A, 15 C, 16 G, 10 T; 0 other;

Alignment Scores:
Pred. No.:                228          Length:          51
Score:                    23.00        Matches:         5
Percent Similarity:       100.00%      Conservative:    0
Best Local Similarity:    100.00%      Mismatches:      0
Query Match:              100.00%      Indels:          0
DB:                       22           Gaps:            0

US-09-856-070-25 (1-5) x AAS60687 (1-51)

Qy       1 MetLeuArgLeuGln 5
           ||||||||||||||||
Db      19 ATGCTCAGGCTTCAG 33

RESULT 4
AAI77674
ID   AAI77674 standard; DNA; 51 BP.
XX
AC   AAI77674;
XX
DT   09-NOV-2001  (first entry)
XX
DE   Human silent SNP containing nucleic acid SEQ:4615.
XX
KW   Human; single nucleotide polymorphism; SNP; genome, gene therapy,
KW   protein therapy, vaccine, probe, diagnostic assay; detection;
KW   quantitation, restorative therapy; polymorphic; ds.
XX
OS   Homo sapiens
XX
PN   WO200140521-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32758
XX
PR   30-NOV-1999;   99US-0168138.
PR   29-NOV-2000; 2000US-0726173.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-356160/37.
XX
PT   Polymorphic nucleic acid sequences, useful in genetic testing and
PT   therapy -
XX
PS   Claim 1, Page 1323, 2653pp; English.
XX
CC   AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC   sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC   AAM53114 to AAM53329 represent peptides related to human polymorphic
CC   polynucleotide sequences. The sequences can be used in gene and protein
CC   therapy, and in vaccine production. (I) and the polypeptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of polymorphic polypeptides.
CC   For example, (I) may be used to treat disorders by rectifying mutations
CC   or deletions in a patient's genome that affect the activity of
CC   polypeptides by expressing inactive proteins or to supplement the
CC   patients own production of polypeptide. Additionally, (I) and its
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays to detect and quantitate the presence of similar nucleic acids
CC   in samples, and therefore which patients may be in need of restorative
CC   therapy. The polypeptides encoded by (I) may be used as antigens in the
CC   production of antibodies specific for polymorphic polypeptides. The
CC   antibodies may also be used to down regulate expression and activity.
CC   The antibodies may also be used as diagnostic agents for detecting the
CC   presence of polymorphic polypeptides in samples.
XX
SQ   Sequence 51 BP, 11 A, 15 C, 14 G, 11 T, 0 other;

Alignment Scores:
Pred. No.:                228          Length:          51
Score:                    23.00        Matches:         5
Percent Similarity:       100.00%      Conservative:    0
Best Local Similarity:    100.00%      Mismatches:      0
Query Match:              100.00%      Indels:          0
DB:                       22           Gaps:            0

US-09-856-070-25 (1-5) x AA177674 (1-51)

Qy       1 MetLeuArgLeuGln 5
           ||||||||||||||||
Db      18 ATGCTGAGGCTACAG 32

RESULT 5
ABN34918
ID   ABN34918 standard; DNA; 60 BP.
XX
AC   ABN34918;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:7666.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB01903.
XX
PR   28-JUL-2000; 2000US-221607P.
PR   02-MAY-2001; 2001US-287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of
```

PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 7666; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 18 A; 20 C; 17 G; 13 T; 0 other;

Alignment Scores:

Pred. No.:	272	Length:	60
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-070-25 (1-5) x ABN34918 (1-60)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      18 ATGCTCAGGCTTCAG 32
```

RESULT 6
ABN43764
ID ABN43764 standard; DNA; 60 BP.
XX
AC ABN43764;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:16512.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 16512; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 15 A; 13 C; 15 G; 17 T; 0 other;

Alignment Scores:

Pred. No.:	272	Length:	60
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-070-25 (1-5) x ABN43764 (1-60)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      18 ATGTTGAGATTACAG 32
```

RESULT 7
AAT25114/c
ID AAT25114 standard; DNA; 73 BP.
XX
AC AAT25114;
XX
DT 22-OCT-1996 (first entry)
XX
DE Human gene signature HUMGS07270.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX

PP 12-NOV-1998; 98JP-0355504.
XX
PA (MAIS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Identifying gene signatures in 3' directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Claim 1; Page 1772; 2245pp; Japanese.
XX
CC A single stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues, synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 73 BP; 16 A; 17 C; 20 G; 18 T; 2 other;

Alignment Scores:

Pred. No.:	337	Length:	73
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-09-856-070-25 (1-5) x AAT25114 (1 73)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db      42 ATGCTGAGATTACAC 28
```

RESULT 8
AAS04515
ID AAS04515 standard; cDNA; 91 BP.
XX
AC AAS04515;
XX
DT 07-SEP-2001 (first entry)
XX
DE Gene expression profile sequence #15.
XX
KW Gene expression profile; hypersensitivity; DNA microarray;
KW liver toxicity; hepatitis; tumour formation; immunosuppression;
KW renal toxicity; glomuleritis; neurotoxicity; leukaemia; dementia;
KW peripheral neuropathy, hypertension, hypotension, myelosuppression;
KW retinopathy, inflammation, sensitisation; ss.
XX
OS Homo sapiens.
XX
PN WO200132928-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30474.
XX
PR 05-NOV-1999; 99US-0163998
PR 11-APR-2000; 2000US-0196571.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
XX
PI Farr S;
XX
DR WPI; 2001-428806/34.
XX
PT Identifying hypersensitivity in a subject by obtaining a gene
PT expression profile of hypersensitivity associated genes and detecting a
PT predetermined pattern of gene expression of hypersensitivity associated
PT genes -
XX
PS Claim 24; Page 138; 222pp; English.
XX
CC The sequence represents a cDNA from a gene associated with
CC hypersensitivity to a agent, the sequence was detected in a sample
CC by use of a DNA microarray containing genes from a gene expression
CC profile thought to be associated with hypersensitivity to an agent. The
CC invention relates to methods of obtaining a gene expression profile of
CC genes associated with hypersensitivity to an agent involving comparing
CC the gene expression profile of cells treated with the agent with the gene
CC expression profile of cells not treated with the agent, and determining
CC the genes that have altered expression due to exposure to the
CC agent. Hypersensitivity in a subject can then be detected by comparing
CC the gene expression profile of the subject with that associated with
CC the hypersensitivity, usually by hybridisation of a sample of mRNA
CC or cDNA from the subject to a DNA microarray containing genes from the
CC hypersensitivity profile. The genes in the profiles are associated
CC with liver toxicity (e.g. hepatitis), tumour formation,
CC immunosuppression, renal toxicity (e.g. glomuleritis), neurotoxicity,
CC leukaemia, dementia, peripheral neuropathy, hyper/hypotension,
CC myelosuppression, retinopathy, inflammation, and sensitisation.
XX
SQ Sequence 91 BP; 19 A; 33 C; 11 G; 28 T; 0 other;

Alignment Scores:

Pred. No.:	427	Length:	91
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-856-070-25 (1-5) x AAS04515 (1-91)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db      33 ATGCTCAGGCTTCAA 47
```

RESULT 9
AAS04706/c
ID AAS04706 standard; cDNA; 91 BP.
XX
AC AAS04706;
XX
DT 07-SEP-2001 (first entry)
XX
DE Gene expression profile sequence #206.
XX
KW Gene expression profile; hypersensitivity; DNA microarray;
KW liver toxicity; hepatitis; tumour formation; immunosuppression;
KW renal toxicity; glomuleritis; neurotoxicity; leukaemia; dementia;
KW peripheral neuropathy, hypertension; hypotension, myelosuppression;
KW retinopathy; inflammation; sensitisation; ss.
XX
OS Homo sapiens.
XX
PN WO200132928-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30474.

XX
PR 05-NOV-1999; 99US-0165398.
PR 11-APR-2000; 2000US-0196571.
XX
PA (PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.
XX
PI Farr S;
XX
DR WPI; 2001-328806/34.
XX
PT Identifying hypersensitivity in a subject by obtaining a gene
PT expression profile of hypersensitivity associated genes and detecting a
PT predetermined pattern of gene expression of hypersensitivity associated
PT genes -
XX
PS Claim 24; Page 194; 222pp; English.
XX
CC The sequence represents a cDNA from a gene associated with
CC hypersensitivity to a agent, the sequence was detected in a sample
CC by use of a DNA microarray containing genes from a gene expression
CC profile thought to be associated with hypersensitivity to an agent. The
CC invention relates to methods of obtaining a gene expression profile of
CC genes associated with hypersensitivity to an agent involving comparing
CC the gene expression profile of cells treated with the agent with the gene
CC expression profile of cells not treated with the agent, and determining
CC the genes that have altered expression due to exposure to the
CC agent. Hypersensitivity in a subject can then be detected by comparing
CC the gene expression profile of the subject with that associated with
CC the hypersensitivity, usually by hybridisation of a sample of mRNA
CC or cDNA from the subject to a DNA microarray containing genes from the
CC hypersensitivity profile. The genes in the profiles are associated
CC with liver toxicity (e.g. hepatitis), tumour formation,
CC immunosuppression, renal toxicity (e.g. glomuleritis), neurotoxicity,
CC leukaemia, dementia, peripheral neuropathy, hyper/hypotension,
CC myelosuppression, retinopathy, intlammation, and sensitisation.
XX
SQ Sequence 91 BP; 28 A; 11 C; 33 G; 19 T; 0 other;

Alignment Scores:

Pred. No.:	427	Length:	91
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-856-070-25 (1-5) x AAS04706 (1-91)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db      59 ATGCTCAGGCTTCAA 45
```

RESULT 10
AAC14334/c
ID AAC14334 standard; cDNA; 103 BP.
XX
AC AAC14334;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 18409.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
PS Claim 1; SEQ ID 18409; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 103 BP; 23 A; 25 C; 31 G; 24 T; 0 other;

Alignment Scores:

Pred. No.:	488	Length:	103
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-856-070-25 (1-5) x AAC14334 (1-103)

```
Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||||
Db      23 ATGCTGAGATTACAG 9
```

RESULT 11
AAC17085/c
ID AAC17085 standard; cDNA; 112 BP.
XX
AC AAC17085;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 21160.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.

```
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
PS   Claim 1; SEQ ID 21160; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors
XX
SQ   Sequence 112 BP; 16 A; 36 C; 27 G; 33 T; 0 other;

Alignment Scores:
Pred. No.:                535          Length:          112
Score:                    23.00        Matches:         5
Percent Similarity:       100.00%      Conservative:    0
Best Local Similarity:    100.00%      Mismatches:      0
Query Match:              100.00%      Indels:          0
DB:                       21           Gaps:            0

US-09-856-070-25 (1-5) x AAG17065 (1-112)

Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      45 ATGCTGAGGCTGCAG 31

RESULT 12
AAA45803/c
ID   AAA45803 standard; cDNA; 112 BP.
XX
AC   AAA45803;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human secreted expressed sequence tag SEQ ID NO:2378.
XX
KW   Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
KW   expressed sequence tag; EST; probe, chemotactic, proliferative;
KW   immunomodulatory, haematopoietic, chemokinetic, analgesic; haemostatic;
KW   thrombolytic, antiinflammatory, cytostatic, antibacterial; antifungal;
KW   antiviral; antidiabetic, antiasthmatic, vulnerary, antiparkinsonian;
KW   antiulcer; osteopathic, neuroprotective, nootropic; antipsoriatic;
KW   cerebroprotective; anticonvulsant; antidepressant, gene therapy;
KW   vaccine; autoimmune disorder, multiple sclerosis, allergic condition;
KW   insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW   central nervous system disorder; Alzheimer's disease; stroke;
KW   Parkinson's disease; Huntington's disease, coagulation disorder;
KW   haemophilia; thrombosis; inflammatory disorder; Cronn's disease;
KW   tumour; infection; depression, psoriasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200021991 A1.
XX
PD   20-APR-2000.
XX
PF   15-OCT-1999;   99WO-US24208
XX
PR   15-OCT-1998;   98US-0104436.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  McCoy JM,  LaValle ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Bowman MR;
XX
DR   WPI; 2000-317938/27.
XX
PT   Isolated polynucleotides, and encoded proteins, comprising secreted
PT   expressed sequence tags (sESTs), useful for treating various disorders
PT   such as autoimmune, infectious, and central nervous system disorders -
XX
PS   Claim 1, Page 776, 803pp; English.
XX
CC   AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC   sequence tags (sESTs), isolated from human, mouse, chicken and rat
CC   tissue sources. The sESTs can have a range of activities depending on
CC   the tissues they were isolated from. The activities include:
CC   chemotactic; proliferative; immunomodulatory; haematopoietic;
CC   chemokinetic, analgesic, haemostatic, thrombolytic, antiinflammatory;
CC   cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC   antiasthmatic; vulnerary; antiulcer; osteopathic, neuroprotective;
CC   nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC   anticonvulsant, and antidepressant. The sESTs can be used for gene
CC   therapy and in vaccines. The sESTs are useful as probes for the
CC   identification and isolation of full-length cDNAs and genomic DNA
CC   molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC   are useful in assays for determining biological activity and raising
CC   antibodies. They may be useful for treatment of autoimmune disorders
CC   (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC   (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC   osteoporosis, osteoarthritis, central nervous system disorders
CC   (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC   disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC   disease), tumours, bacterial, fungal or viral infections, depression and
CC   psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 112 BP; 31 A; 24 C; 22 G; 35 T; 0 other;

Alignment Scores:
Pred. No.:                535          Length:          112
Score:                    23.00        Matches:         5
Percent Similarity:       100.00%      Conservative:    0
Best Local Similarity:    100.00%      Mismatches:      0
Query Match:              100.00%      Indels:          0
DB:                       21           Gaps:            0

US-09-856-070-25 (1-5) x AAA45803 (1-112)

Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      81 ATGTTAAGGCTTCAA 67

RESULT 13
ABK76832
ID   ABK76832 standard; DNA; 129 BP.
XX
AC   ABK76832;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Bacillus licheniformis genomic sequence tag (GST) #4123.
XX
KW   Differential gene expression; genomic sequenced tag; GST;
KW   altered culture condition; environmental stress;
KW   physiological provocation; ds.
XX
OS   Bacillus licheniformis.
XX
PN   WO200229113-A2.
XX
PD   11-APR-2002.
XX
```

```
PT   05-OCT-2001; 2001WO-US31437.
XX
PR   06-OCT-2000; 2000US-0680598.
PR   27-MAR-2001; 2001US-2795260.
XX
PA   (NOVO ) NOVOZYMES BIOTECH INC.
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Berka R, Clausen IG;
XX
DR   WPI; 2002-416684/44.
XX
PT   Monitoring differential expression of several genes in first Bacillus
PT   cell relative to expression of same genes in one or more second
PT   Bacillus cells, by using substrate containing Bacillus genomic
PT   sequenced tag array
XX
PS   Claim 4; SEQ ID NO 4124; 200pp; English.
XX
CC   The invention describes a method of monitoring differential expression of
CC   genes in a first Bacillus cell relative to expression of the genes in
CC   other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC   isolated from Bacillus cells to a substrate containing array of Bacillus
CC   genomic sequenced tags (GST), examining the array, and determining
CC   relative gene expression by an observed hybridisation reporter signal of
CC   a spot in the array. The method is useful for measuring the expression of
CC   genes in a first Bacillus cell relative to expression of the same genes
CC   in one or more second Bacillus cells. The method is useful for monitoring
CC   global expression of several genes from a Bacillus cell, discovering new
CC   genes, identifying possible functions of unknown open reading frames and
CC   monitoring gene copy number variation and stability. Monitoring changes
CC   in expression of genes may be used to provide a representation of the way
CC   in which Bacillus cells adapt to changes in culture conditions,
CC   environmental stress or other physiological provocation. Extensive
CC   follow-up characterisation is unnecessary, when one spot on an array
CC   equals one gene or one open reading frame, since sequence information is
CC   available. This sequence represents a genomic sequence tag (GST) used in
CC   the method of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 129 BP; 27 A; 40 C; 29 G; 33 T; 0 other;

Alignment Scores:
Pred. No.:                623             Length:         129
Score:                    23.00           Matches:        5
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       24              Gaps:           0

US-09-856-070-25 (1-5) x ABK76832 (1-129)

Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      66 ATGTTACGACTTCAA 80

RESULT 14
AAH37077/c
ID   AAH37077 standard; cDNA; 134 BP.
XX
AC   AAH37077;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:4159.
XX
KW   Human; colon cancer; colon cancer antigen, diagnosis, detection,
KW   colorectal carcinoma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG77670.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers
XX
PS   Claim 1; Page 6010; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAB37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7953 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence 134 BP; 39 A; 33 C; 35 G; 19 T; 8 other;

Alignment Scores:
Pred. No.:                649             Length:         134
Score:                    23.00           Matches:        5
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       22              Gaps:           0

US-09-856-070-25 (1-5) x AAH37077 (1-134)

Qy       1 MetLeuArgLeuGln 5
           |||||||||||||||
Db      62 ATGCTCCGTCTTCAG 48

RESULT 15
ABA35126
ID   ABA35126 standard; DNA; 139 BP.
XX
AC   ABA35126;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #13592 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID No 13592; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 139 BP; 42 A; 36 C; 23 G; 38 T; 0 other;

Alignment Scores:

Pred. No.:	675	Length:	139
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-856-070-25 (1-5) x ABA35126 (1-139)

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Qy       1 MetLeuArgLeuGln 5
           ||||||||||||||||
Db      60 ATGCTTAGGTTGCAG 74
```

Search completed: January 16, 2003, 17:19:52
Job time : 82.9821 secs